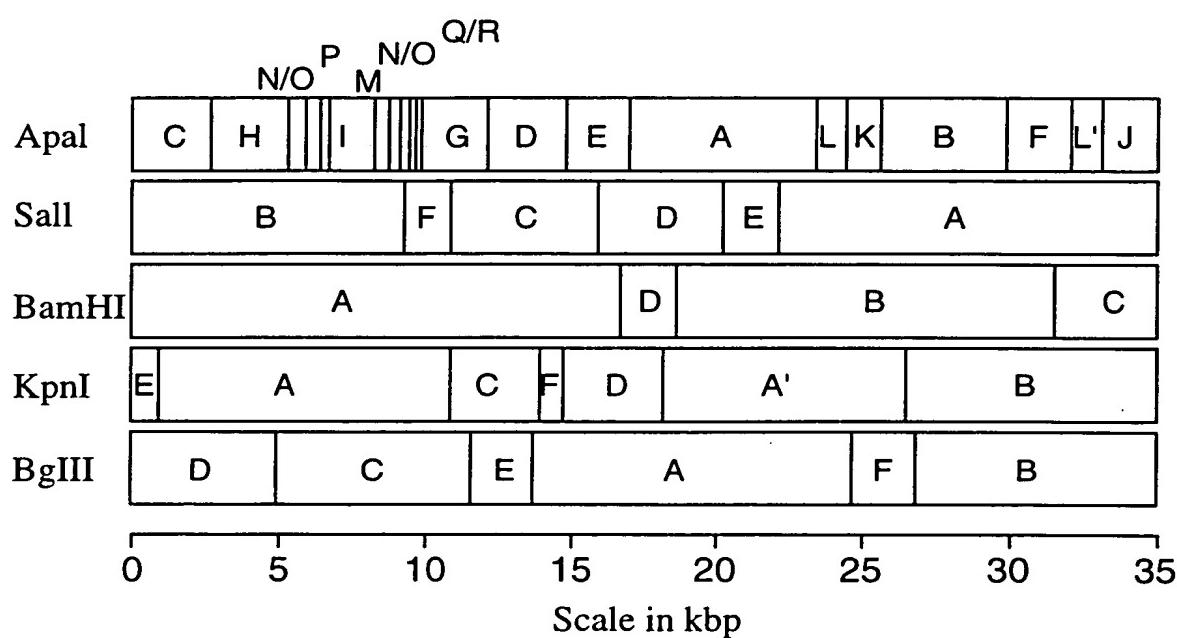


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Fig 1.

Restriction enzyme maps of the PAV3 genome



APPROVED	G.G. FIG.	
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Fig 2.

Total sequence of the PAV Major Late Promoter cassette including the added nucleotides 5' (upstream) of the USF.

Nucleotide base count: 76 A 143 C 187 G 96 T Total 502 bp

1	GGTCCGGGG TCGTCGGGT	AGAGGTAGAG	GGCCCAGTCG	GAGATGAAGG CACGCCCA
61	GGCAGGGACG AAGCTGGCGA	CCTGGGAGGG	GTAGCGGGTCG	<u>TGGGCACTA</u> ATGGCGAGGC
121	CTGCTCGAGC GTGTGGAGAC	AGAGGTCTCT	GTCGTCCGCG	TCCAGGAAGT GGATTGGTGG
181	CCAGTGGTAG TCCACGTGAC	CGGCTTGCGG	GTCGGGGGT	<u>ATAAAAGGCC</u> CGGGCCGGGG
241	TGCCTGGCCG TC <u>A<u>GTGCTT</u></u>	CGCAGGCCCT	GTCACCGGAG	TCCGGTCTC CGGGGTCTCG
301	CGCTGGGCT GCATCTGTGG	TCCCGGGAGTC	TTCAGGTCTT	TGTTGAGGAG GTACTCCCTGA
361	TCGCTGTCCC AGTACTTGGC	<u>GTGTTGGAAAG</u>	CCGGTCTGTAT	<u>CGCGATCCTC</u> CTGCTGTGTGC
421	AGCGCTTCGG CAAACACGGC	CACCTGCTCT	TCGGACCCGG	CGAACGGTTC GACGAAGGGCG
481	TCTAGCCAGC AACAGTCGCA	<u>AG</u>		

The Upstream Stimulatory Factor (USF) and TATA motif are in **bold**. The complete leader sequence is italicised with the cap site and splice sites between the individual leaders indicated by double underlining or single underlining respectively.

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Fig 3.

Individual sequences of the Promoter cassette components:

I. The 5' (upstream) sequence included in the long cassette.

```

1      GGTGCCGCGG TCGTCGGCGT AGAGGATGAG GGCCCAGTCG GAGATGAAGG CACCGGCCA
61     GGCAGGACG AAGCTGGCGA CCTGCGAGGG TAGCGGTG TTGGGCACTA ATGGCGAGGC
121    CTGCTCGAGC GTGTGGAGAC AGAGGTCCCTC GTCGTCCGCG TCCAGGAAGT GGATTGGTCG
181    CCAGTGGTAG

```

II. Sequence including the USF, TATA motif and sequence to the cap site.

```

1      CCACGTGACC GGCTTGCAGG TCAGGGGGTA TAAAAAGGCGC GGGCCGGGGT GCGTGGCCGT
61     C

```

III. First leader sequence.

```

1      AGTTGCTTCG CAGGCCTCGT CACCGGAGTC CGCGTCTCCG GCGTCTCGCG CTGCGGCTGC
61     ATCTGTGGTC CGGGAGTCTT CAG

```

IV. Second leader sequence.

```

1      GTCCTTGTTG AGGAGGTACT CCTGATCGCT GTCCCAGTAC TTGGCGTGTG GGAAGCCGTC
61     CTGATCG

```

V. Third leader sequence.

```

1      CGATCCTCCT GCTGTTGCAG CGCTTCGGCA AACACGCGCA CCTGCTCTTC GGACCCGGCG
61     AAGCGTTCGA CGAAGGGCGTC TAGCCAGCAA CAGTCGCAAG

```

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Sequence of the right hand end of the PAV genome this area being a proposed site for insertion of expression cassettes.

Fig 4.

Nucleotide base count 183 A 255 C 306 G 204 T Total 948 bases

1	CATCATCAAT	AATAACCGC	ACACTTTTAT	TGCCCTTTT	GTGGCGTGGT	GATTGGGGAA
61	GAGGGTGGG	GGGGGGGG	GGTGAATTGGT	GGAGAGGGGT	GTGACCGTAGC	GTGGGAACGT
121	GACGTGGCT	GGAAAATAA	CGTGGCTGG	GAACGGTCAA	AGTCGGAGGG	GCGGGGTCAA
181	AGTCCGAGT	CGGGGGGG	AGCCGGCTGG	CGGGAAATTCC	<u>GGGACTTC</u>	TGGGGGGGTA
241	ATCGTTAACG	CGGAGGGGG	<u>GGAAATTCCGA</u>	TCGGACGATG	<u>Smal</u>	TAAACCGACCG
	HpaI		ECORI			
301	CAGGGCGTGC	CACATCCGGT	GTGGGTATAT	CACCGGGCT	CGGGGTGTC	GCTCACACTC
361	GTCTCGGCCG	TGTACAGAG	AGAGACACTG	AGAGCGAGAC	GAGGAGAAAC	CGAAAGGGGG
421	GCAGGAGGAG	TCACCGGGCC	ATCTTCCCCT	CAGAGCCTC	TCATGGCCCA	CGACCGGACTG
481	CTGCTGCCG	CGGTGGCTGA	CTGTTGCTCG	CCGTGCTCTA	TCTGTACTTC	GCCTACCTCG
541	CGTGGCAGGA	TCGGGACACT	CTTCACACTC	AGGAGGGCGC	CTCTCCCTCGC	TTCTTCATCG
601	GGTCCAACCA	CCAGCCCTGG	TGCCCGGATT	TTGATTGGCA	GGAGCAGGAC	GAGCACACTC
661	ACTAGACGTT	TAGAAAAAAG	ACACACATTG	GAACTCATAT	ATGTCCTGGG	GACGGCATCA
721	GCAGGCCGGT	CTGCTGGTG	CTGGGGGTGA	GAGGCCCTCG	GTAAATTCACT	AGAACCGCAT
781	TCATCTGCCG	CACGTCCCCGA	CATATGGTGC	<u>TGACGTAGA</u>	ACAGCCCAGC	GTGATCCCTT
				StuI		
841	TAATGTGCTA	GTCTACGTGC	CCACTGGGT	SacII		
901	TCAGGGAGG	GATCTGGTCC	GTTTCCAGAC	TGCTGTGTT	GTGCCGACTG	AGCGAGATT
				CTGCTGTTTC	CGGCATCA	

The Inverted Terminal Repeat (ITR) is shown in bold. Enzyme sites of interest are underlined with the enzyme name below. Putative TATA for E4 region is also shown.

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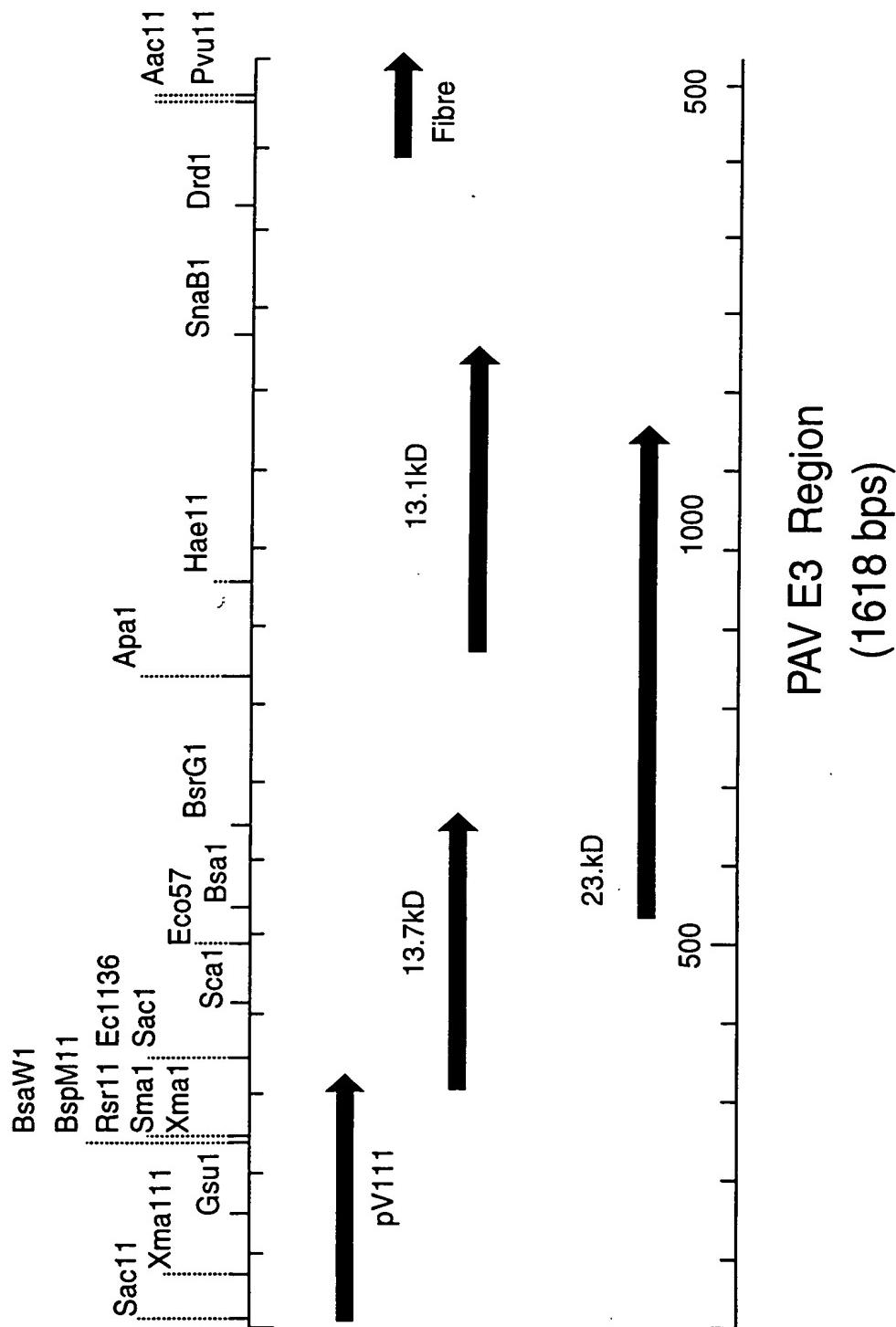
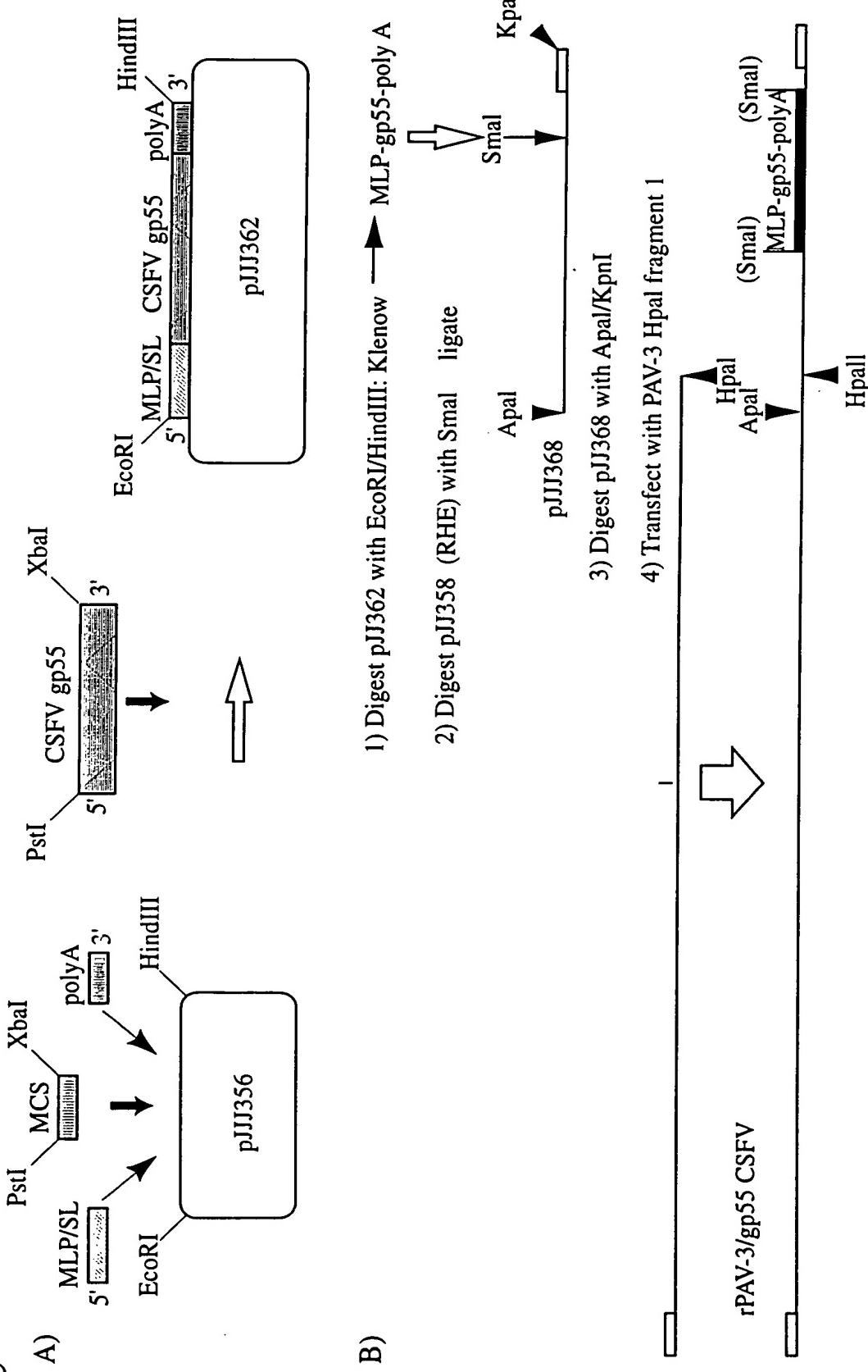


Fig 5.

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Fig 6.



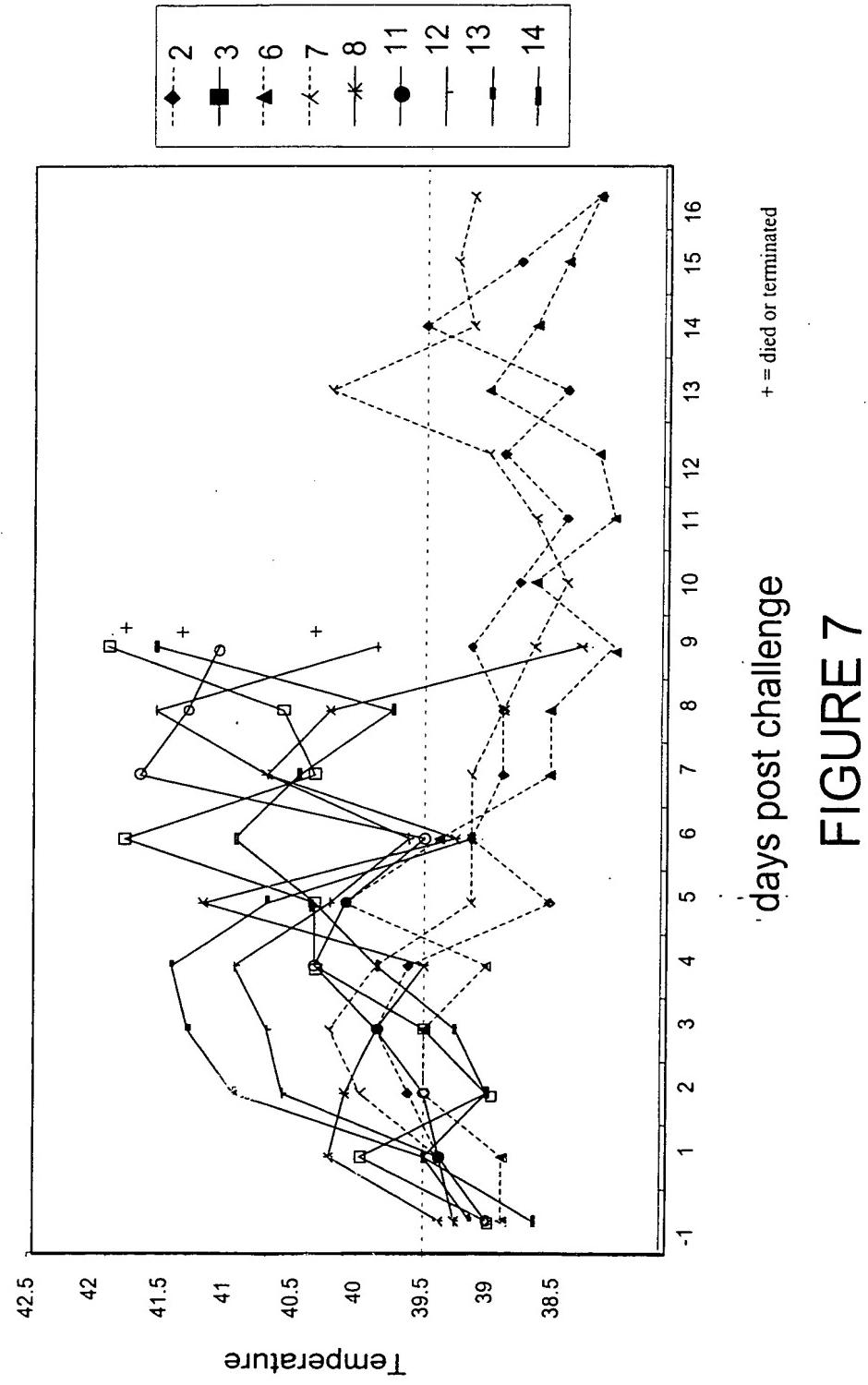


FIGURE 7

APPROVED J.C. FIG.
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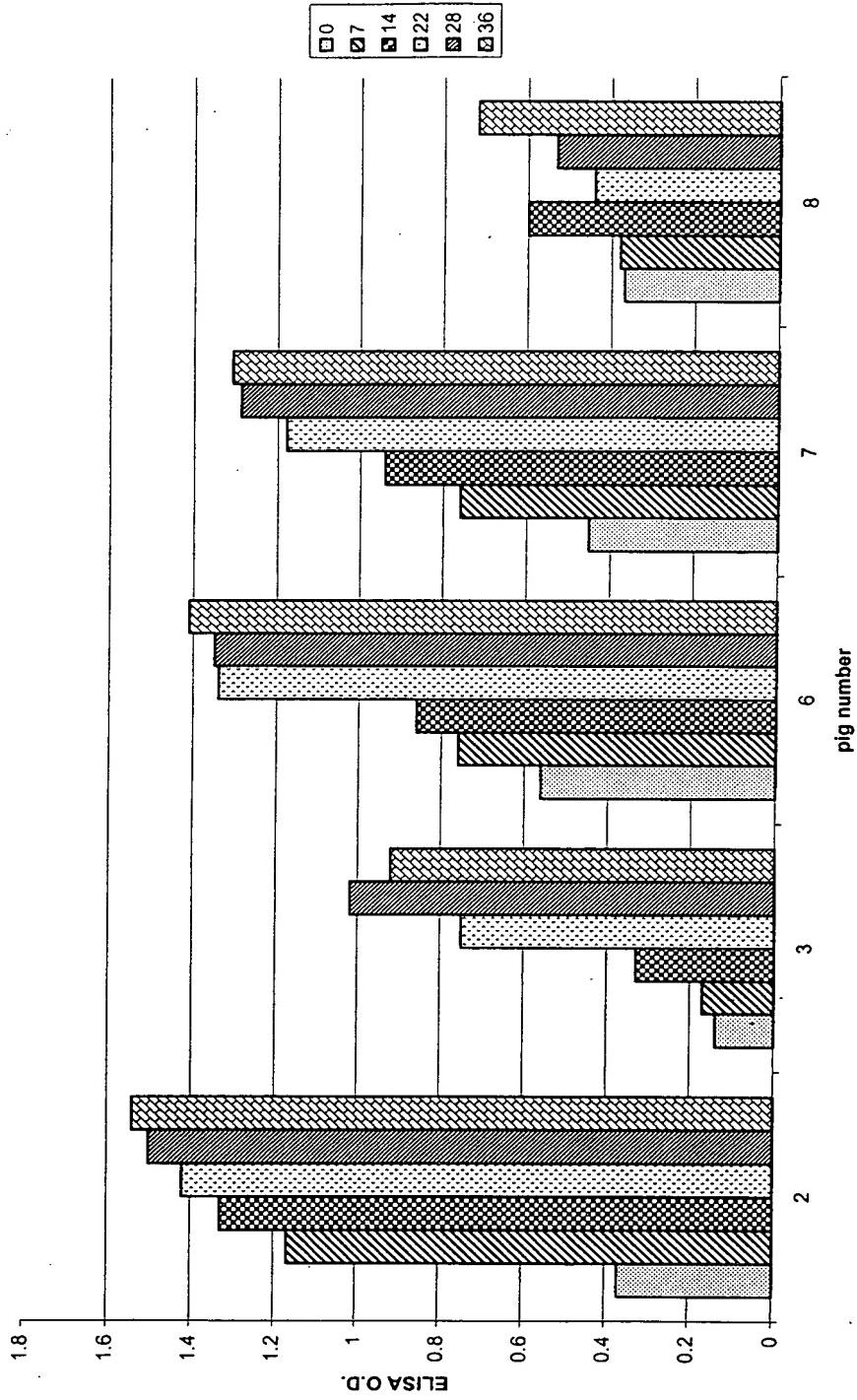


FIGURE 8

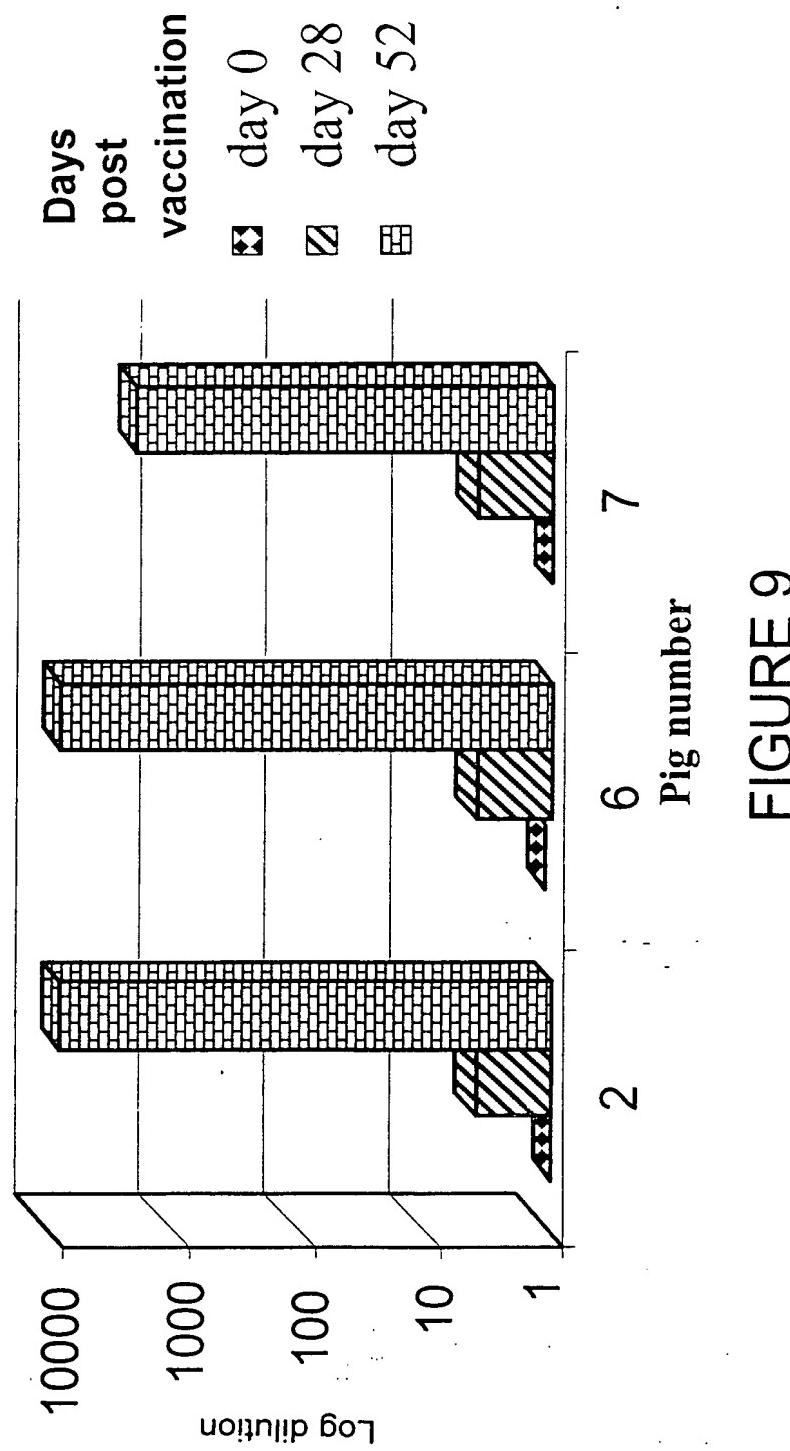
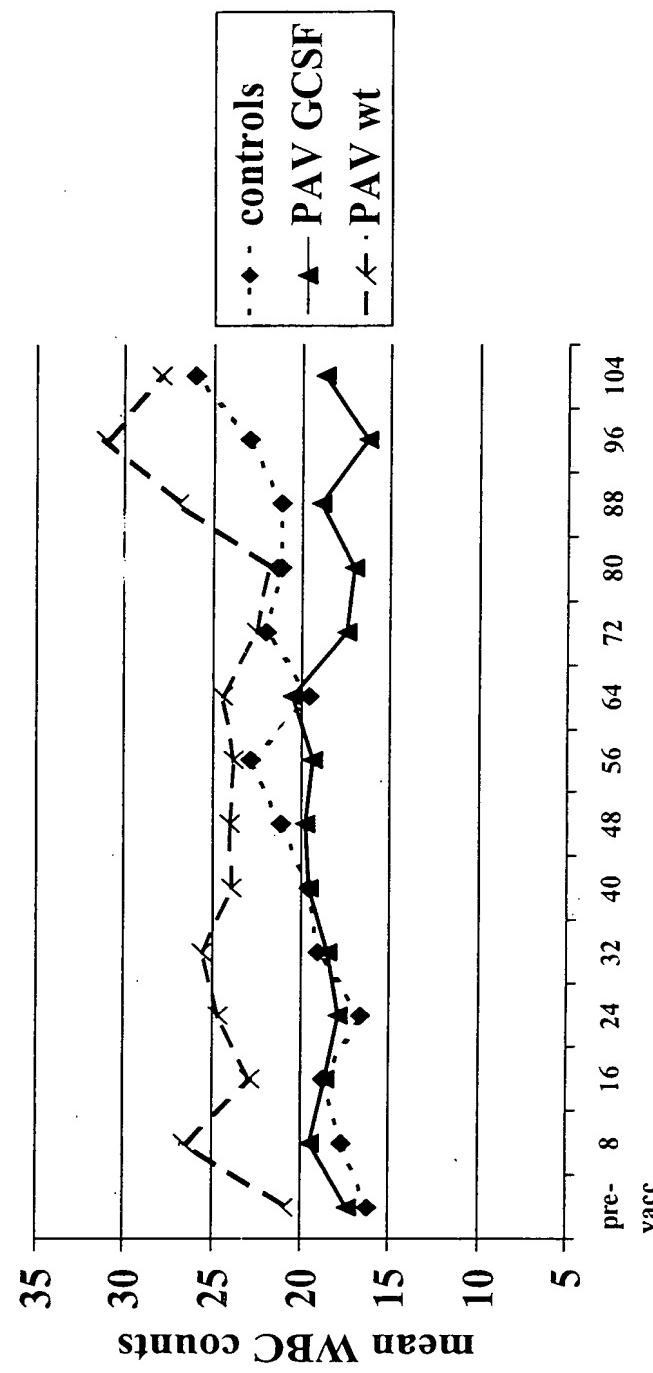


FIGURE 9

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APPROVAL	D.D. FIG.
BY	77120 SUBCLASS
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Hours post vaccination

FIGURE 10

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APPROVED C.G. FIG.
BY CLASS SECCLASS
AFTSMAN

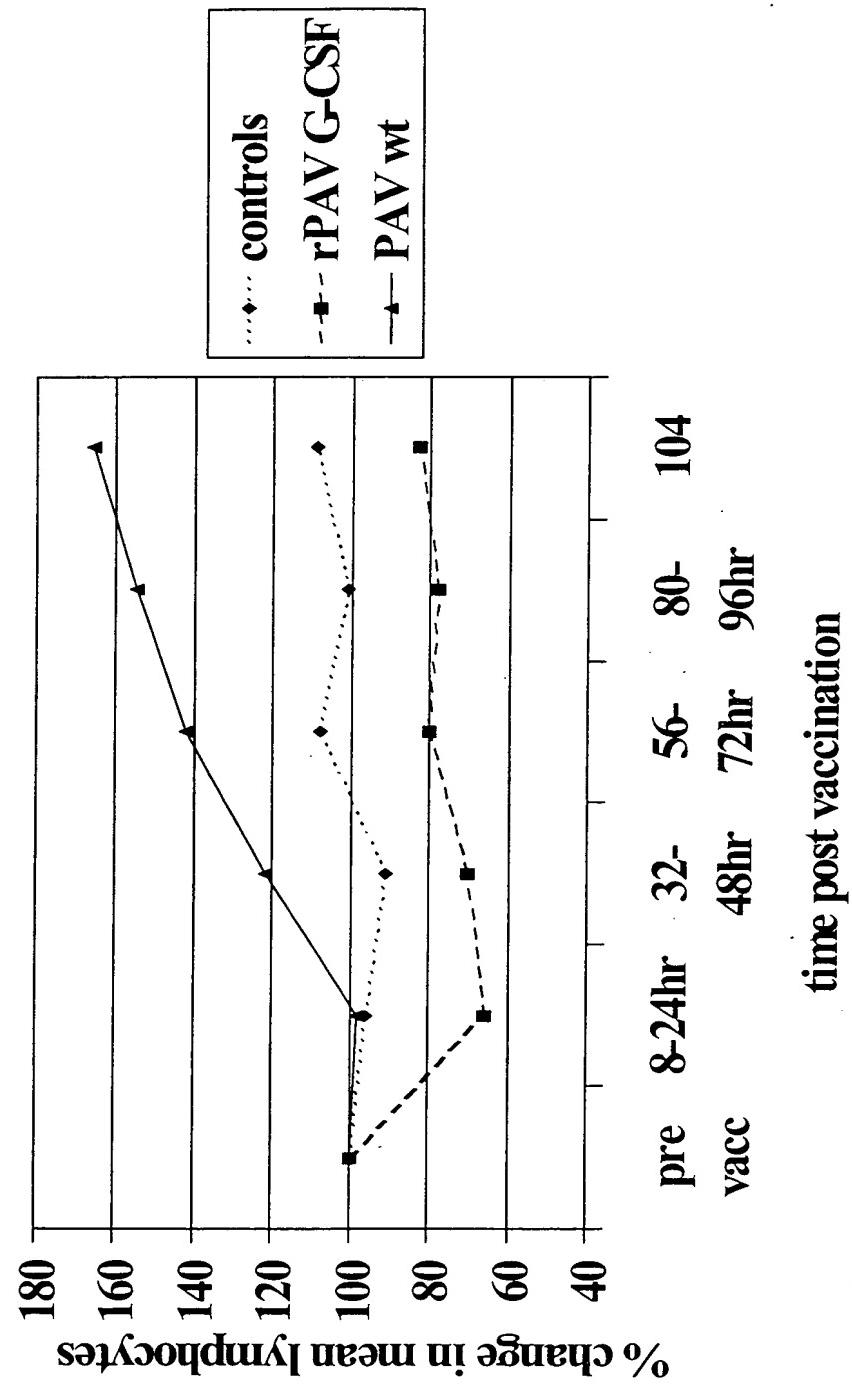


FIGURE 11

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APPROVED: F.G. FIG.
BY: CLASS: 100 CLASS
DRAFTSMAN:

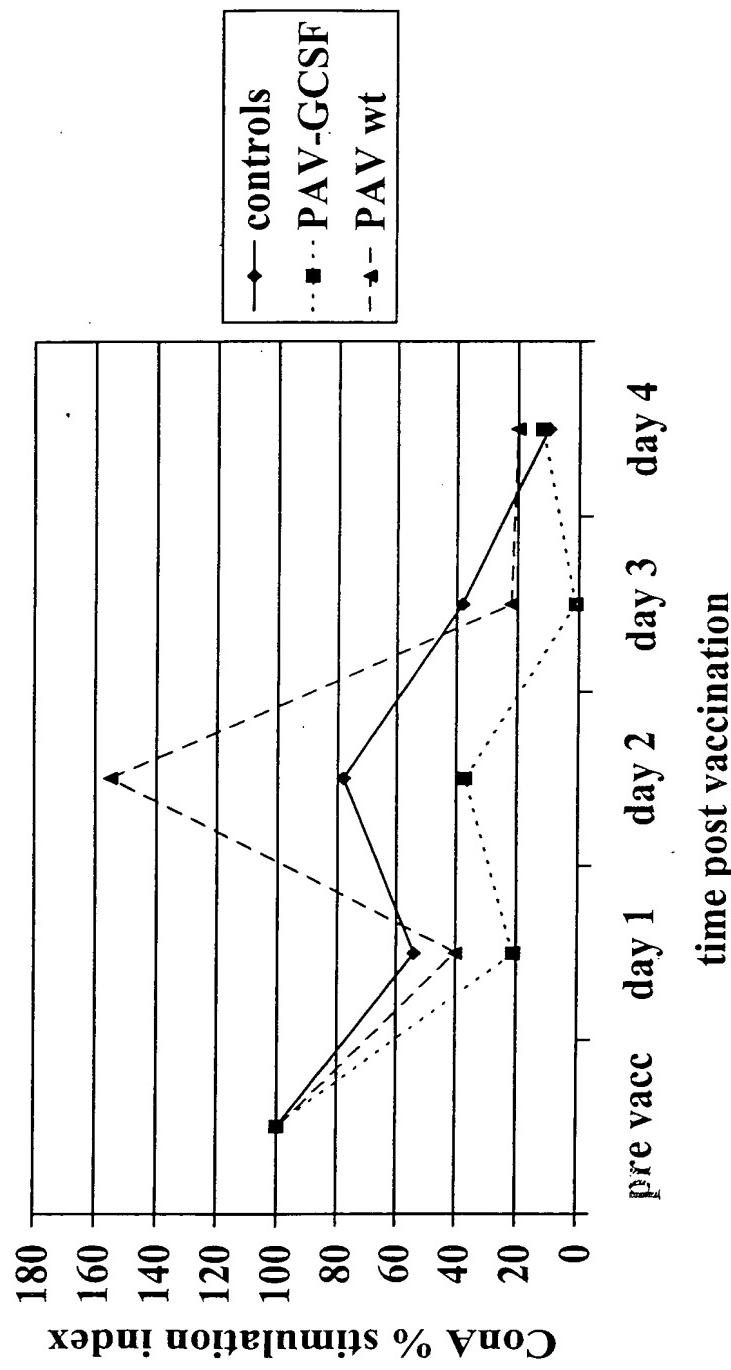


FIGURE 12

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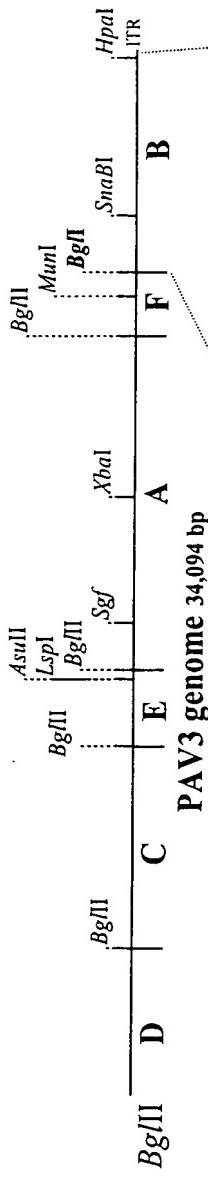


FIG. 13A

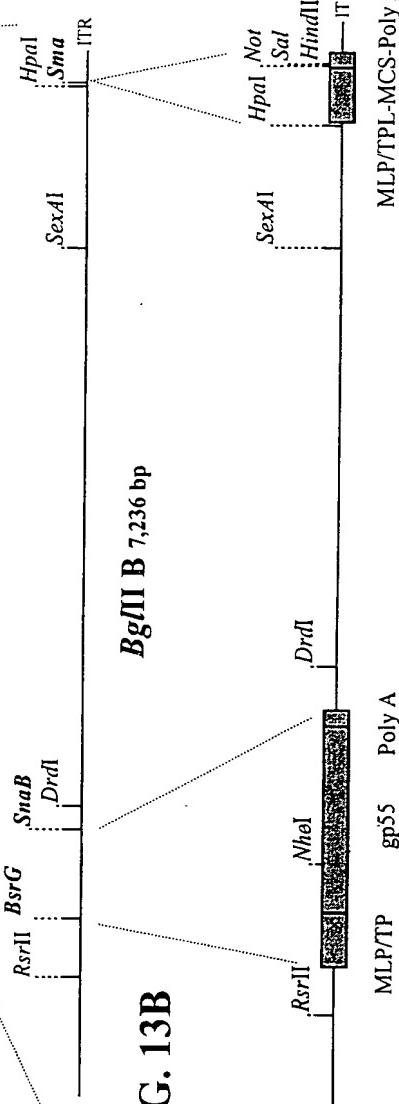


FIG. 13B

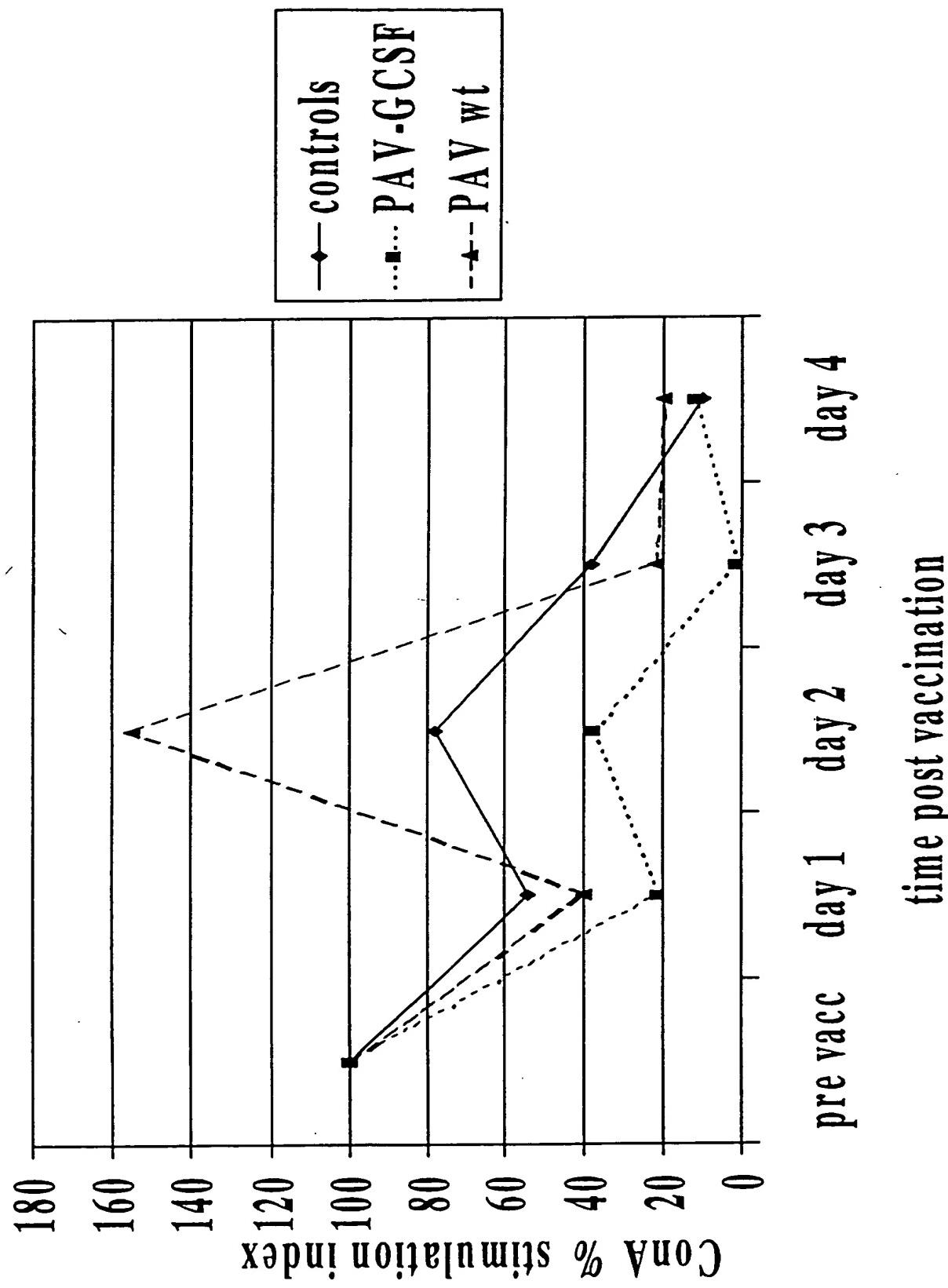


APPROVED	1.C. FIG.
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Fig 14.



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Fig 15.

